

FOIA b 7 - DFOI 2009-0000

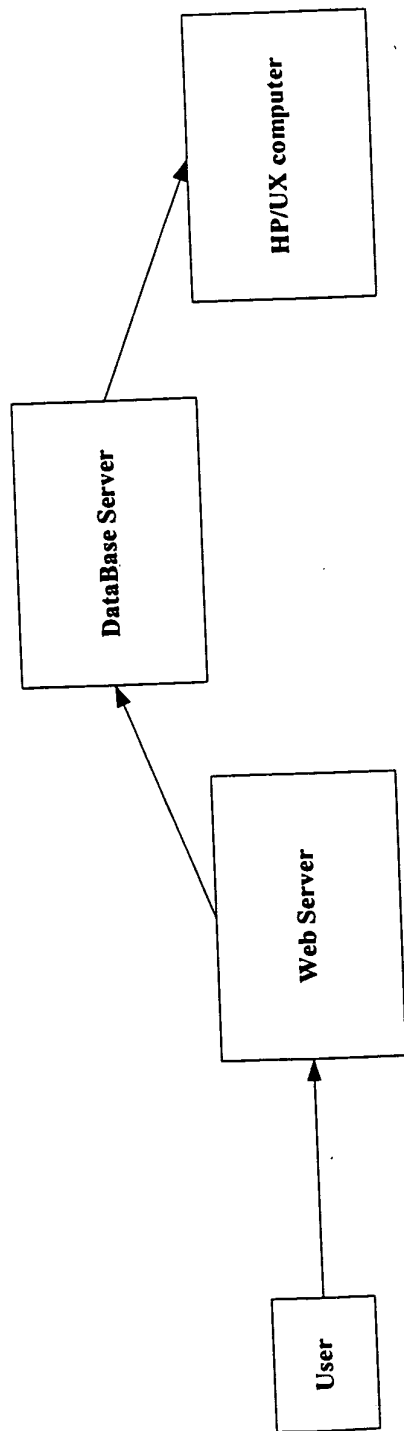


Fig 1

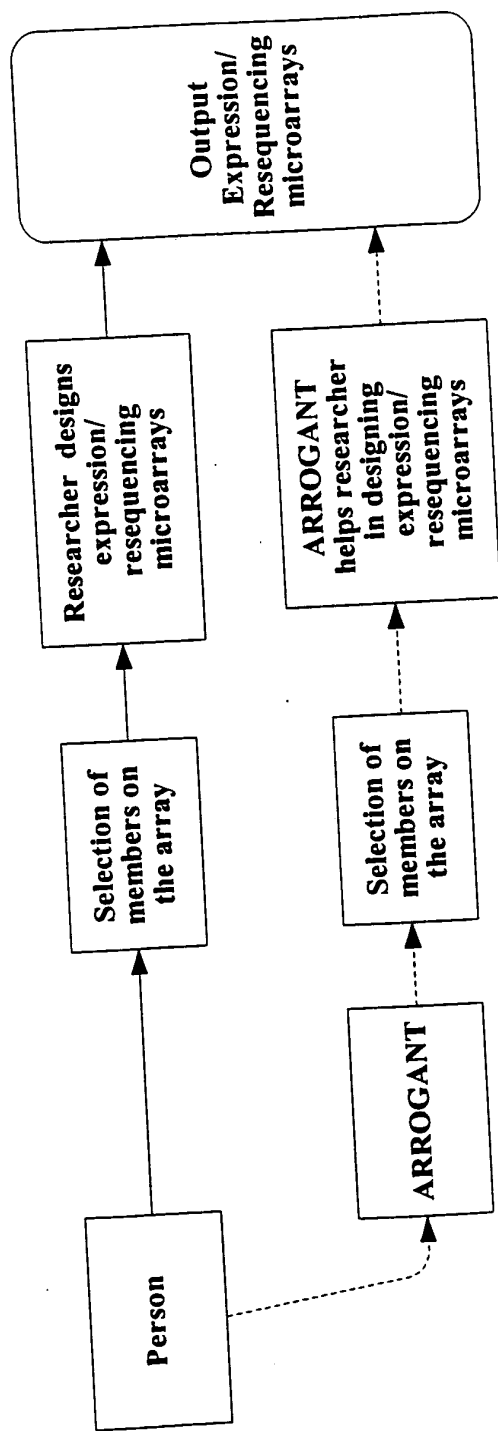


Fig 2

FOI 250 06099860

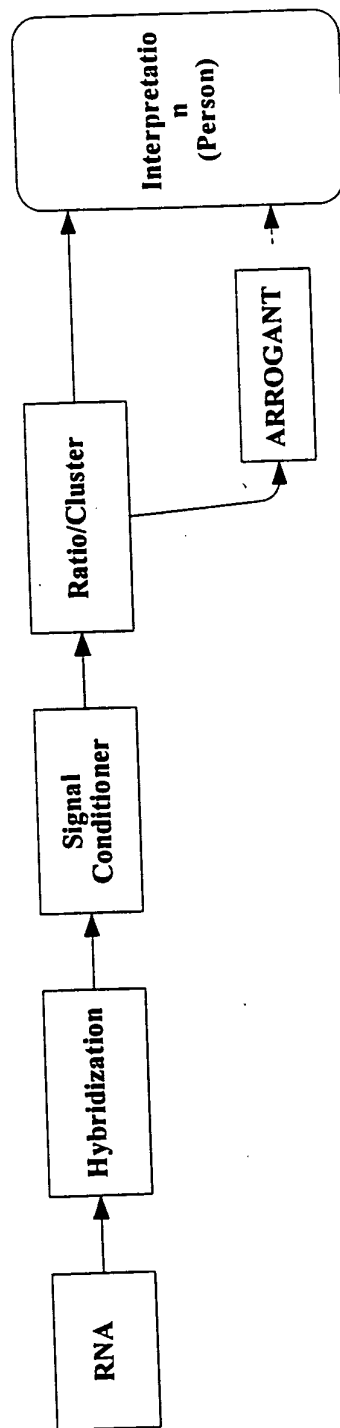


Fig 3

FOI b7E b7C b7D b7F b7G b7H b7I b7J b7K b7L b7M b7N b7O b7P b7Q b7R b7S b7T b7U b7V b7W b7X b7Y b7Z

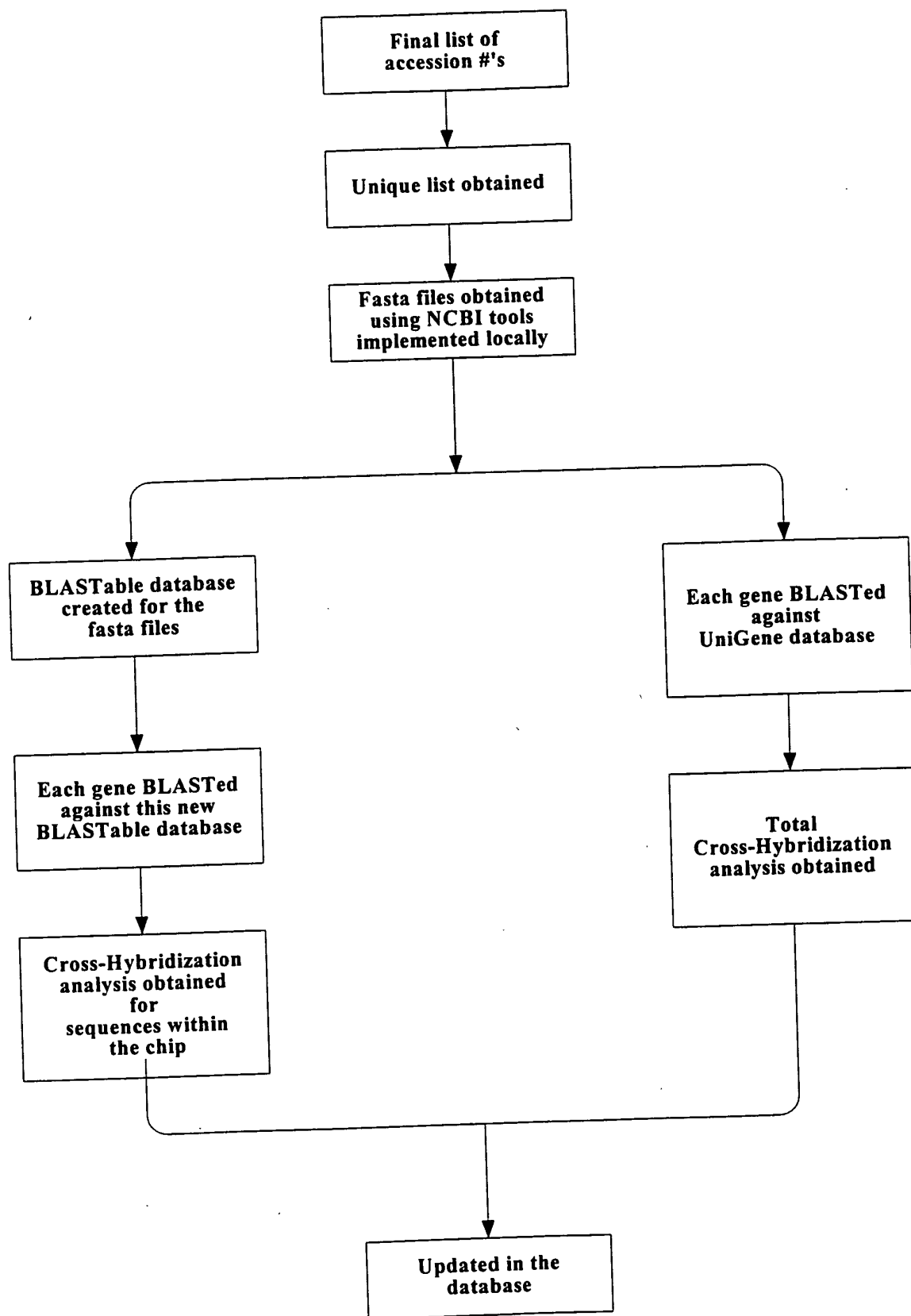


Fig 4

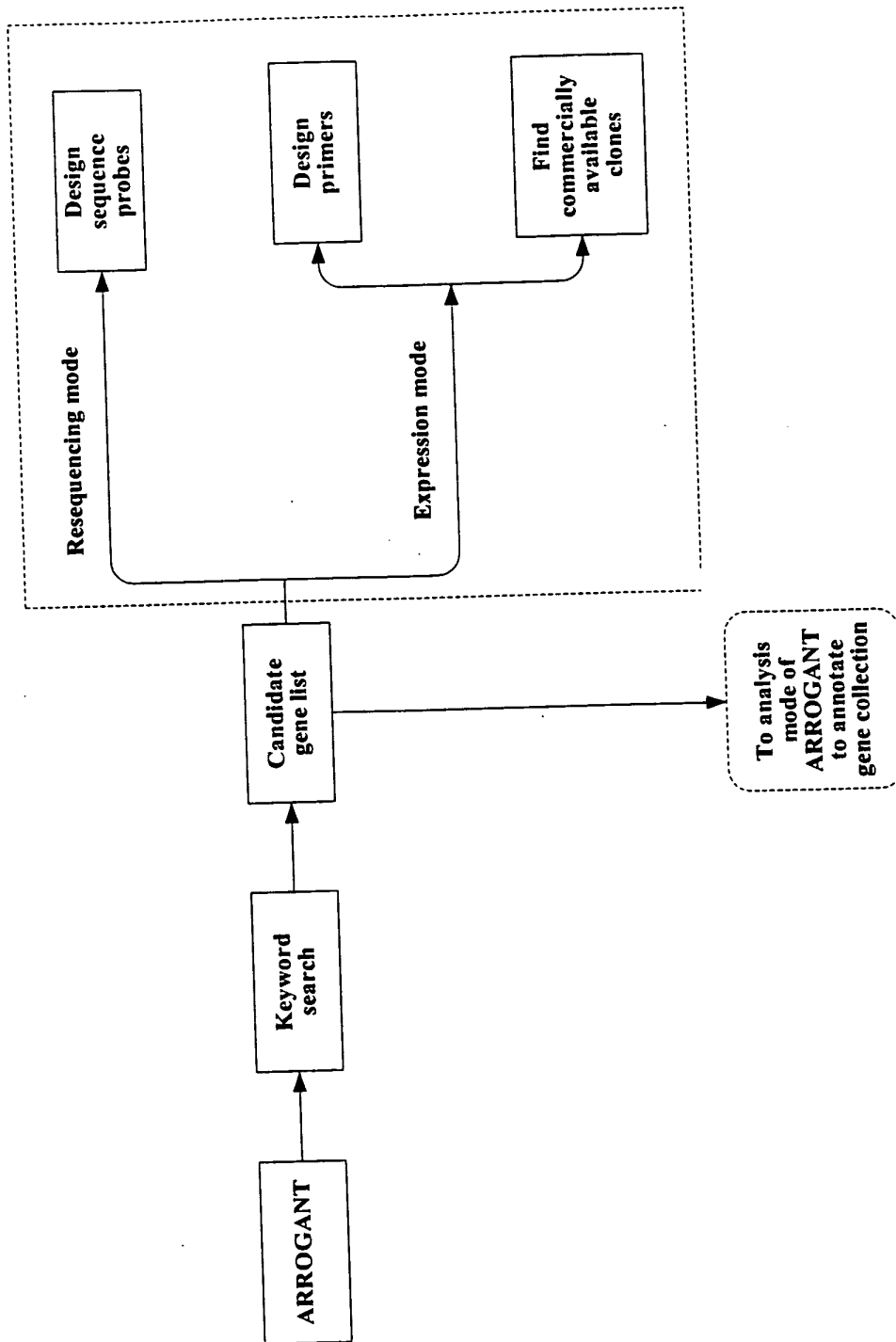


Fig 5

2. **ANTHROCAT - ARRAY ORGANIZING TOOL - Microsoft Internet Explorer**

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Address: <http://anthrocat.swimed.edu/myweb/index.asp>

For more information on any input data item click on the link for examples for help on options

click on Species

User Email: mlh001@uic.edu

Array Name: [pga](#)

Number of Array Members: [10](#) **Use:** [r Resequencing](#) [r Expression](#)

Source: [r PCR Products](#) [r Clones](#) [r Both](#)

Gene Position: [r 3' Exon End Only](#) [r Random Exons](#)

Keywords: [candSac hypotrophy](#)

Databases: [r GenBank](#) [r UniGene](#) [r LocusLink](#) [r KEGG](#) [r KEGG Pathway](#) [r Research Genetics](#)

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Fig 6

FOI250" 00059860

2) Arrogant Results - Macintosh Internet Explorer

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Links My Links My Bookmarks My Recent History My Computer My Recent History My Recent History

Address <http://handgiant.sanmed.edu/mysite/kysearch.asp>

GO: 1 2 3 4 5 6 7 8 9 10

Record	Accession No	Definition	Organism
1	A32415	H.sapiens PAI-2 cDNA in pDBP1.	Homo sapiens
2	AA062310	ml64f06.r1 Stratagene mouse kidney (#937315) Mus musculus cDNA clone IMAGE:516803 5' similar to WP:C40H1.6 CE00114 ;, mRNA sequence.	Mus musculus
3	AA073008	mm94c09.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:536080 5' similar to gb:M22810 Mouse androgen-regulated protein mRNA, complete cds (MOUSE);, mRNA sequence.	Mus musculus
4	AA073010	mm94c11.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:536084 5', mRNA sequence.	Mus musculus
5	AA073011	mm94c12.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:536086 5' similar to gb:X70847	Mus musculus

File Edit View Favorites Tools Help

Back Forward Home Search Favorites History

Links My Links My Bookmarks My Recent History My Recent History My Recent History

Address <http://handgiant.sanmed.edu/mysite/kysearch.asp>

GO: 1 2 3 4 5 6 7 8 9 10

11:30 AM

Fig 7

Form 06053800

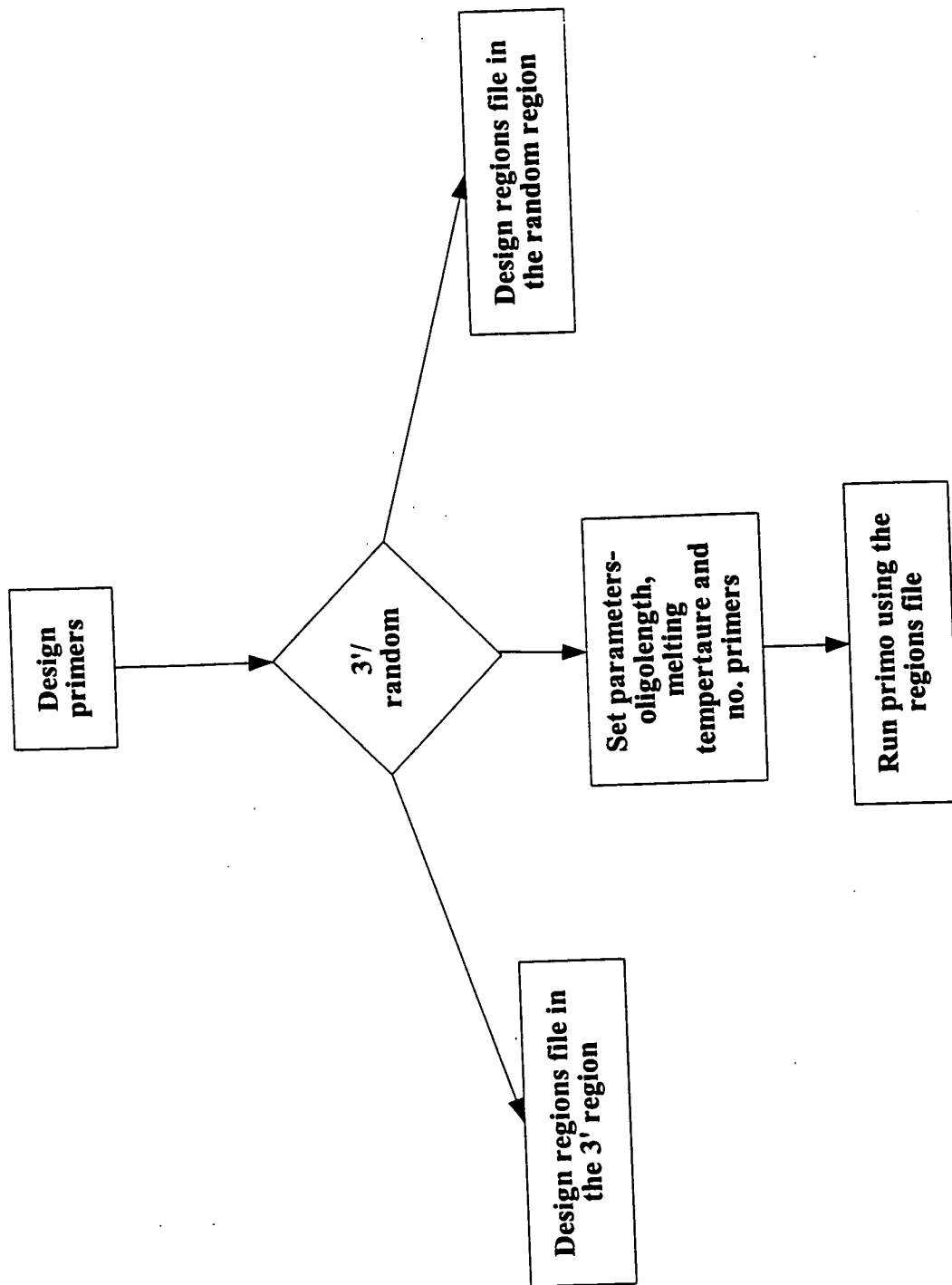


Fig 8

FOI b6 b7C b7D

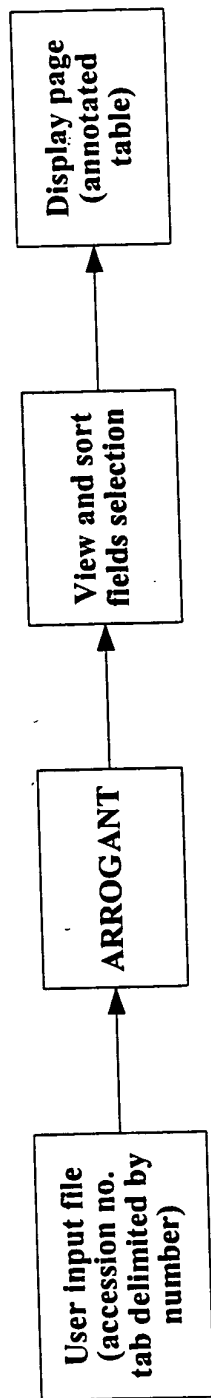


Fig 9

Select the fields you want to view, select how you would like to sort the data and press

Show Collection

<input type="checkbox"/> Accession	<input type="checkbox"/> IMAGE Identifier	<input type="checkbox"/> Alias protein
<input type="checkbox"/> Expression level data	<input type="checkbox"/> Xhyb analysis	<input type="checkbox"/> Phenotype
<input type="checkbox"/> Unique Identifier	<input type="checkbox"/> Issues	<input type="checkbox"/> Phenotype ID/ OMIM ID
<input type="checkbox"/> Title	<input type="checkbox"/> GDB	<input type="checkbox"/> Chromosome
<input type="checkbox"/> PubMed	<input type="checkbox"/> Gene name	<input type="checkbox"/> Map location
<input type="checkbox"/> Related Proteins	<input type="checkbox"/> Gene Function	<input type="checkbox"/> Map link
<input type="checkbox"/> Related Sequences	<input type="checkbox"/> Synonyms	<input type="checkbox"/> Map type
<input type="checkbox"/> Taxonomy	<input type="checkbox"/> Pathway	<input type="checkbox"/> STS- marker name
<input type="checkbox"/> Repeats	<input type="checkbox"/> SNP analysis	<input type="checkbox"/> STS- chromosome
<input type="checkbox"/> Hairpin/Palindrome	<input type="checkbox"/> Unigene ID	<input type="checkbox"/> STS- ID
<input type="checkbox"/> Homology	<input type="checkbox"/> Locus ID	<input type="checkbox"/> Reviewed RefSeq
<input type="checkbox"/> Research Genetics Clone	<input type="checkbox"/> Alias symbol	<input type="checkbox"/> cDNA Source

Sort Preferences

1.
2.
3.
4.
5.

Fig 10

004250" 06059860

Arrogant Server

Welcome to the ARROGANT (ARRAY ORGANIZING Tool) Server, please move back and forth between this page and the earlier page to chose the fields to be viewed and fields to be sorted on.

For more information on any input data field click on that link. For example, for help on Accession click on [Accession](#)

Databases Updated when?

Database	Genbank	Pomposus	LocustHk	Unigene	Research Genetics
Last Updated	2/7/01 8:06:55 AM	1/18/01 8:35:24 AM	2/6/01 8:34:29 AM	1/28/01 8:34:45 AM	1/8/01 8:35:59 AM

Fig 11

Download results table in excel format

Results Table

Record	Accession	Uni ID	Cluster ID	Title	Homologs	Gene Type/Function
1	NM_000236	4557722	Hs.2994	Homo sapiens lipase, hepatic (LIPC), mRNA.	Mm.362 Rn.1195	Summary: LIPC encodes hepatic triglyceride lipase which is expressed in liver. LIPC has dual functions of triglyceride hydrolase and ligand, bridging factor for receptor mediated lipoprotein uptake
2	NM_000023	4506910	Hs.29931	Homo sapiens sarcoglycan, alpha (50kD dystrophin-associated glycoprotein) (SGCA), mRNA.	Mm.18709 Rn.23558	
Summary	239	232	207	232	201	239
Record	Accession	Uni ID	Cluster ID	Title	Homologs	Gene Type/Function

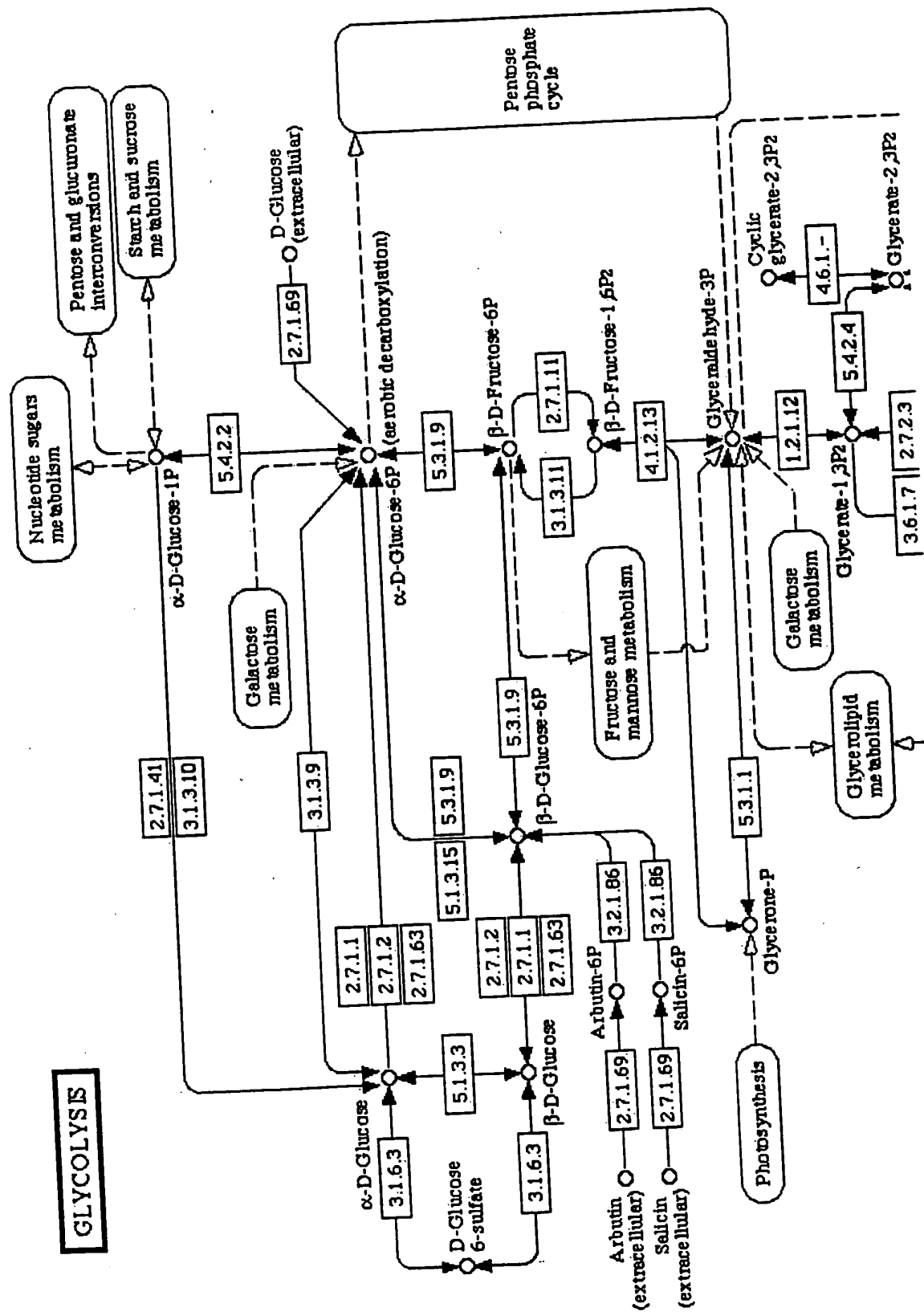


Fig 12

00059860

Column Name	Datatype	Length	Precision	Scale	Allow Null	Default Value
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nid	varchar	10	0	0	✓	((-1))
defn	varchar	255	0	0	✓	((-1))
type	varchar	100	0	0	✓	((-1))
dna	varchar	6	0	0	✓	((-1))
organism	varchar	25	0	0	✓	((-1))
source	varchar	25	0	0	✓	((-1))
keyword	varchar	6	0	0	✓	((-1))
comments	varchar	255	0	0	✓	((-1))
featstuff	varchar	1400	0	0	✓	((-1))
fstart	varchar	10	0	0	✓	((-1))
fend	varchar	10	0	0	✓	((-1))
species	varchar	200	0	0	✓	((-1))
authors	varchar	255	0	0	✓	((-1))
journal	varchar	255	0	0	✓	((-1))
version	varchar	30	0	0	✓	((-1))
reference	varchar	25	0	0	✓	((-1))
title	varchar	100	0	0	✓	((-1))
basepair	varchar	10	0	0	✓	((-1))

Fig 13

104250" 06059850

Metadata	
clusterid	
accession	
type	

UniProt protein	
clusterid	
otherproids	

UniProt	
UG	
express	
locuslink	
title	
gene	
cytoband	
sts	
mqi	
chromosome	

UniProt	
clusterid	
pro org	
pro id	
similarity	

Fig 14

T04250" 06059860

pathway	
	Uniqueld
	pathno
	organism

lookpath	
	pathno
	pathway

kegg	
	Uniqueld
	Locusid
	Organism
	Name
	Defn
	class
	position
	gdb
	ncbi

Fig 16

homoortho	
	Unigid1
	Unigid2
	Locid1
	Locid2
	Acc1
	Acc2

Fig 17

098590.05401
T07250" 06059860

RG_Hs_seq_ver_101100	
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<input type="checkbox"/>	[RG row]
<input type="checkbox"/>	[RG column]
<input type="checkbox"/>	[Insert Size*]
<input type="checkbox"/>	[Cluster ID]
<input type="checkbox"/>	[UG build]
<input type="checkbox"/>	[Clone ID]
<input type="checkbox"/>	Vector
<input type="checkbox"/>	Tissue
<input type="checkbox"/>	Library
<input type="checkbox"/>	Accession
<input type="checkbox"/>	NID
<input type="checkbox"/>	[Gene Name]
<input type="checkbox"/>	[Gene Symbol]
<input type="checkbox"/>	Chromosome
<input type="checkbox"/>	Band
<input type="checkbox"/>	Markers
<input type="checkbox"/>	Col019
<input type="checkbox"/>	Barcode
<input type="checkbox"/>	Antibiotics
<input type="checkbox"/>	[repeat ?]

Fig 18

• •

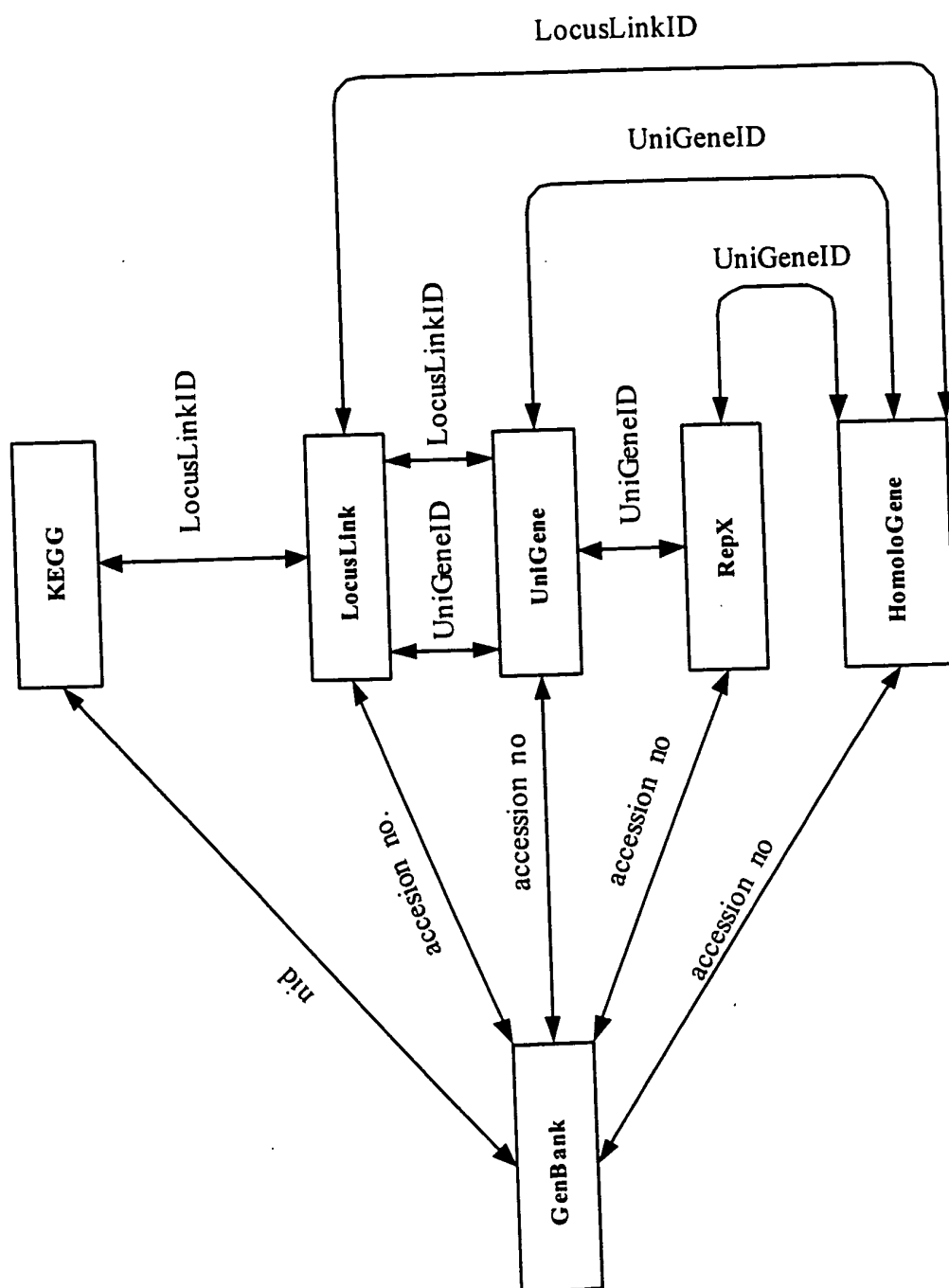


Fig 19

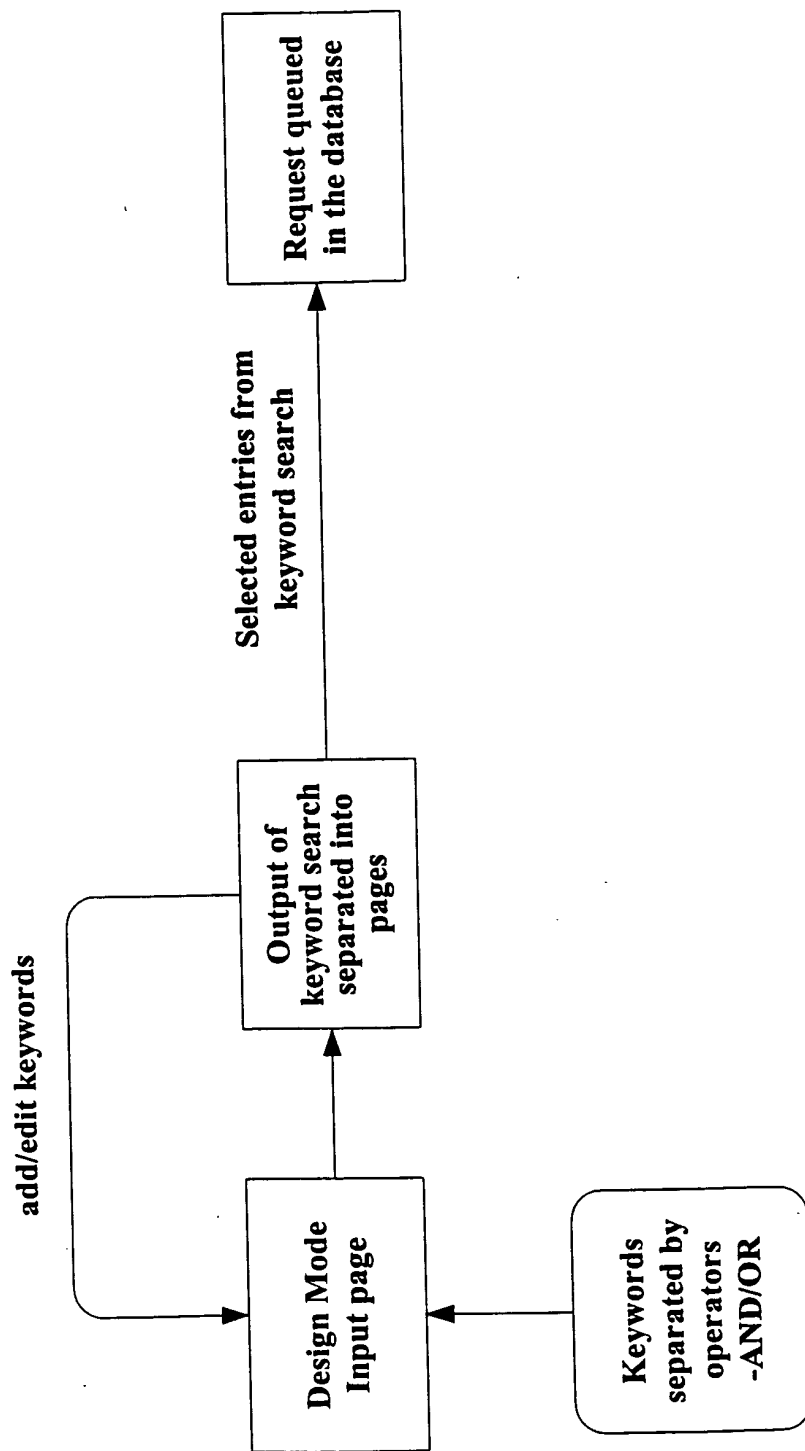
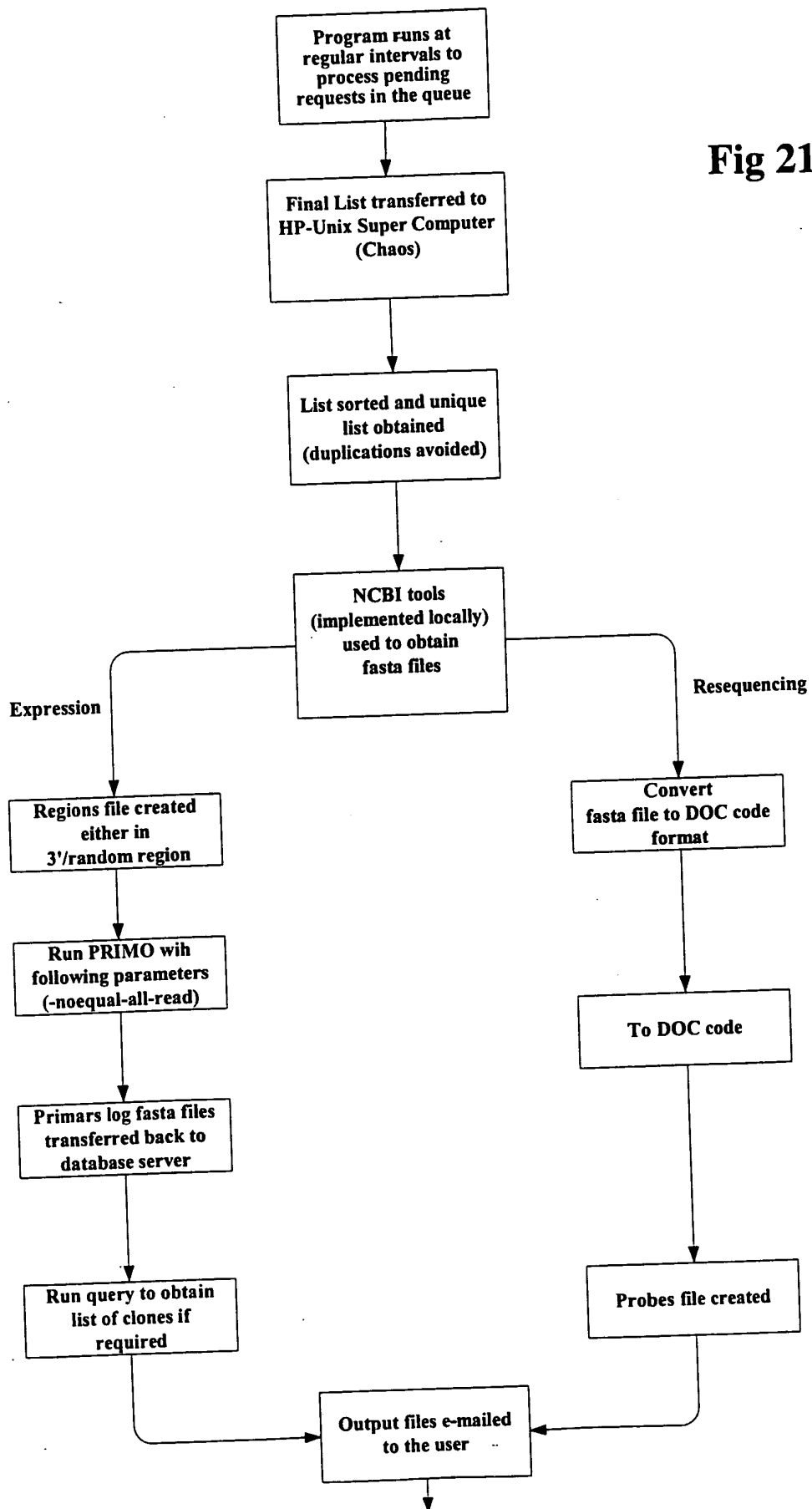


Fig 20

THE UNIVERSITY OF CHICAGO



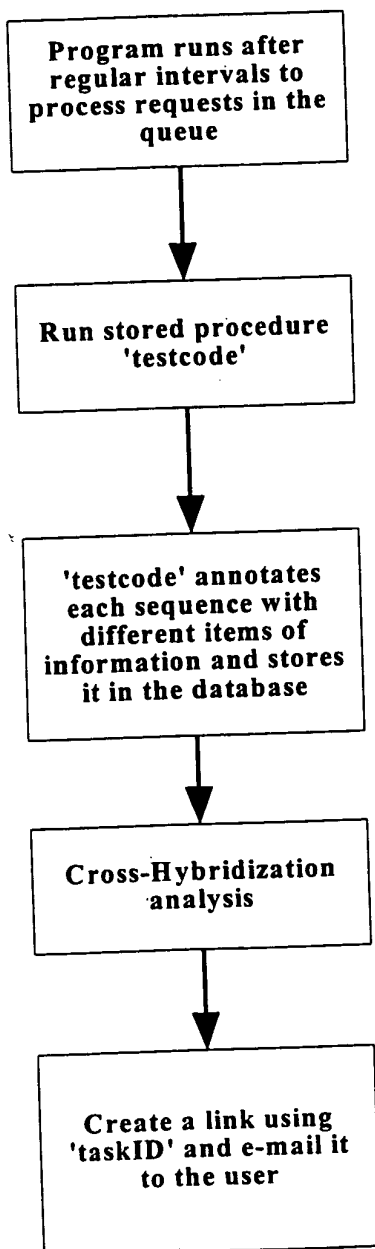
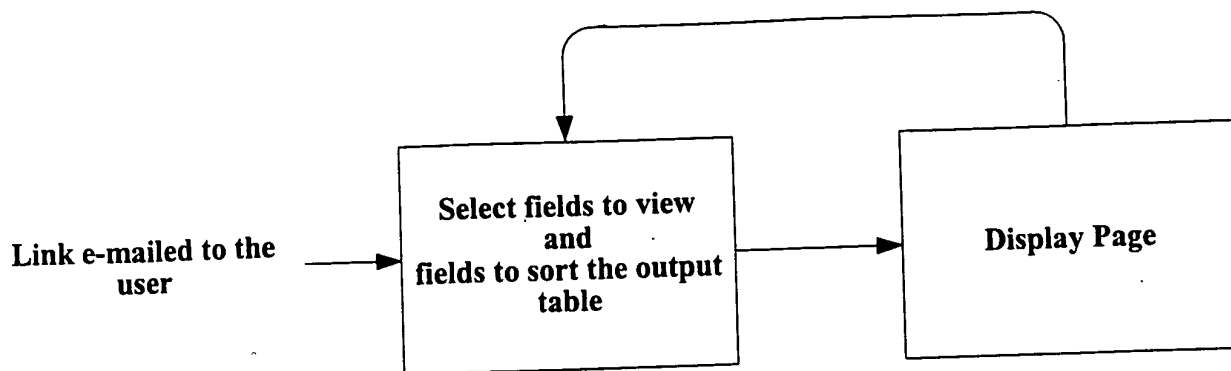


Fig 22

09865090.052401

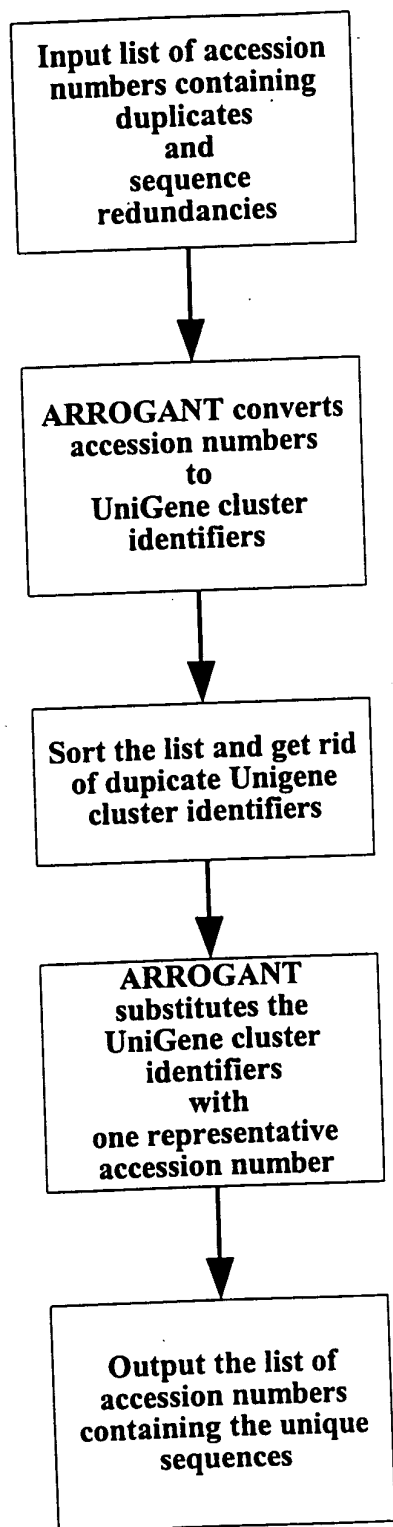


Fig 23

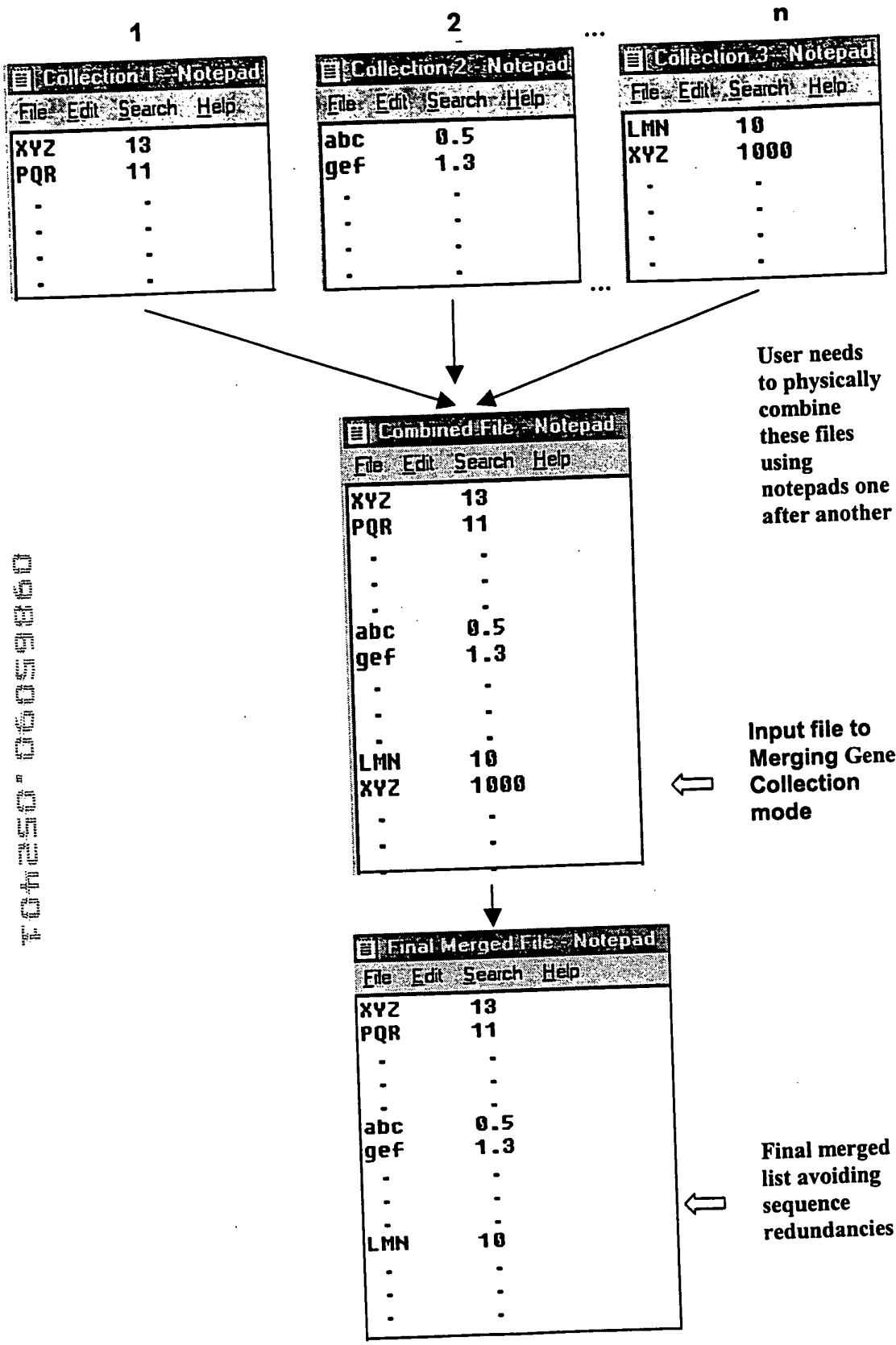


Fig 24

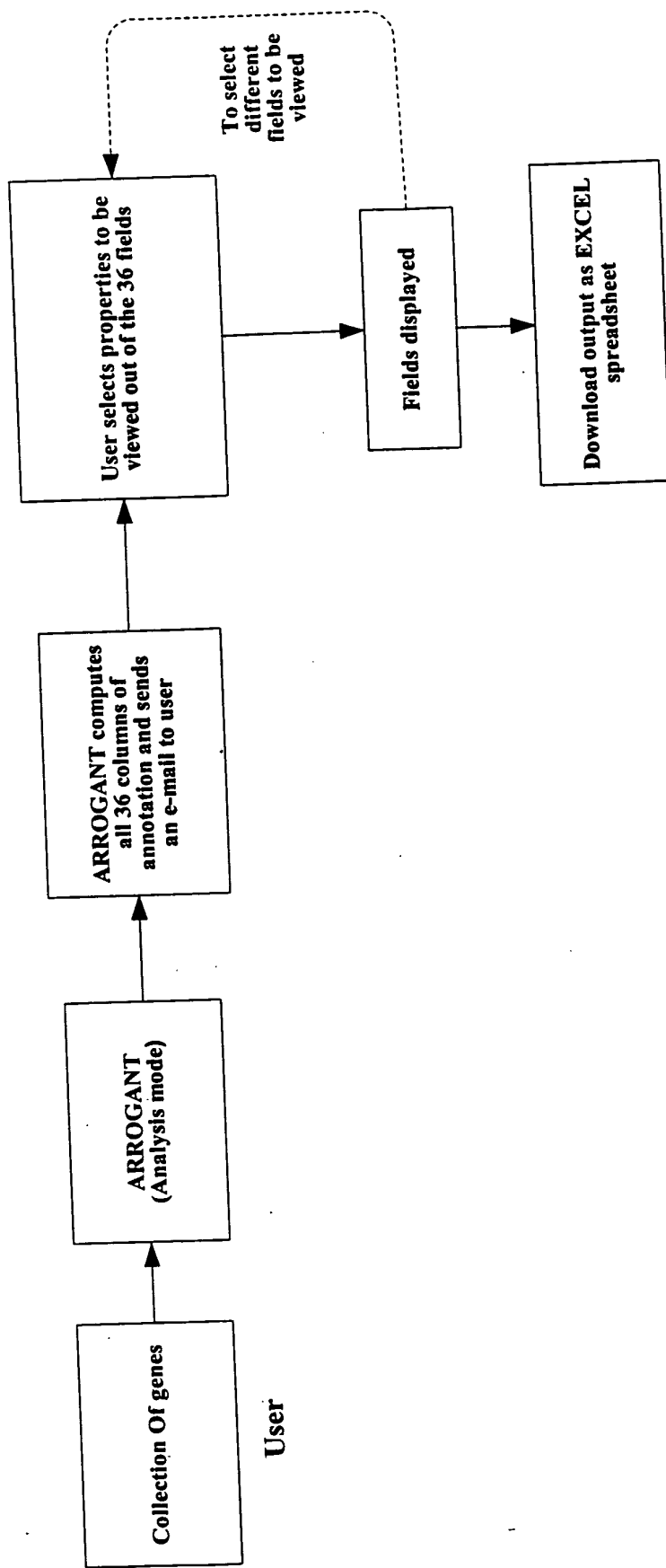


Fig 25

00059860

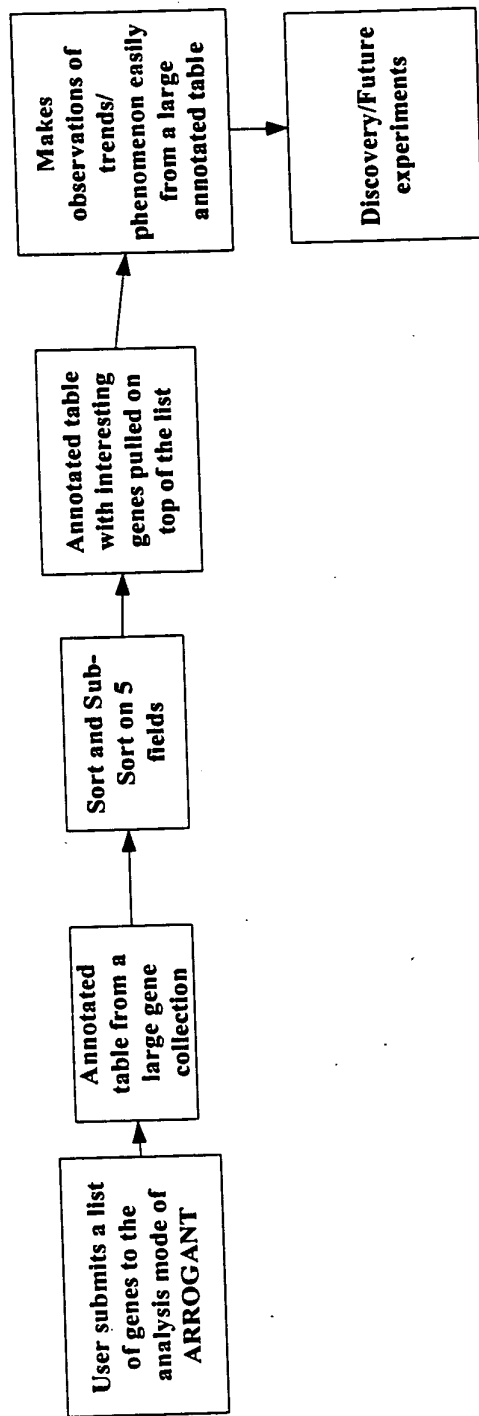


Fig 26

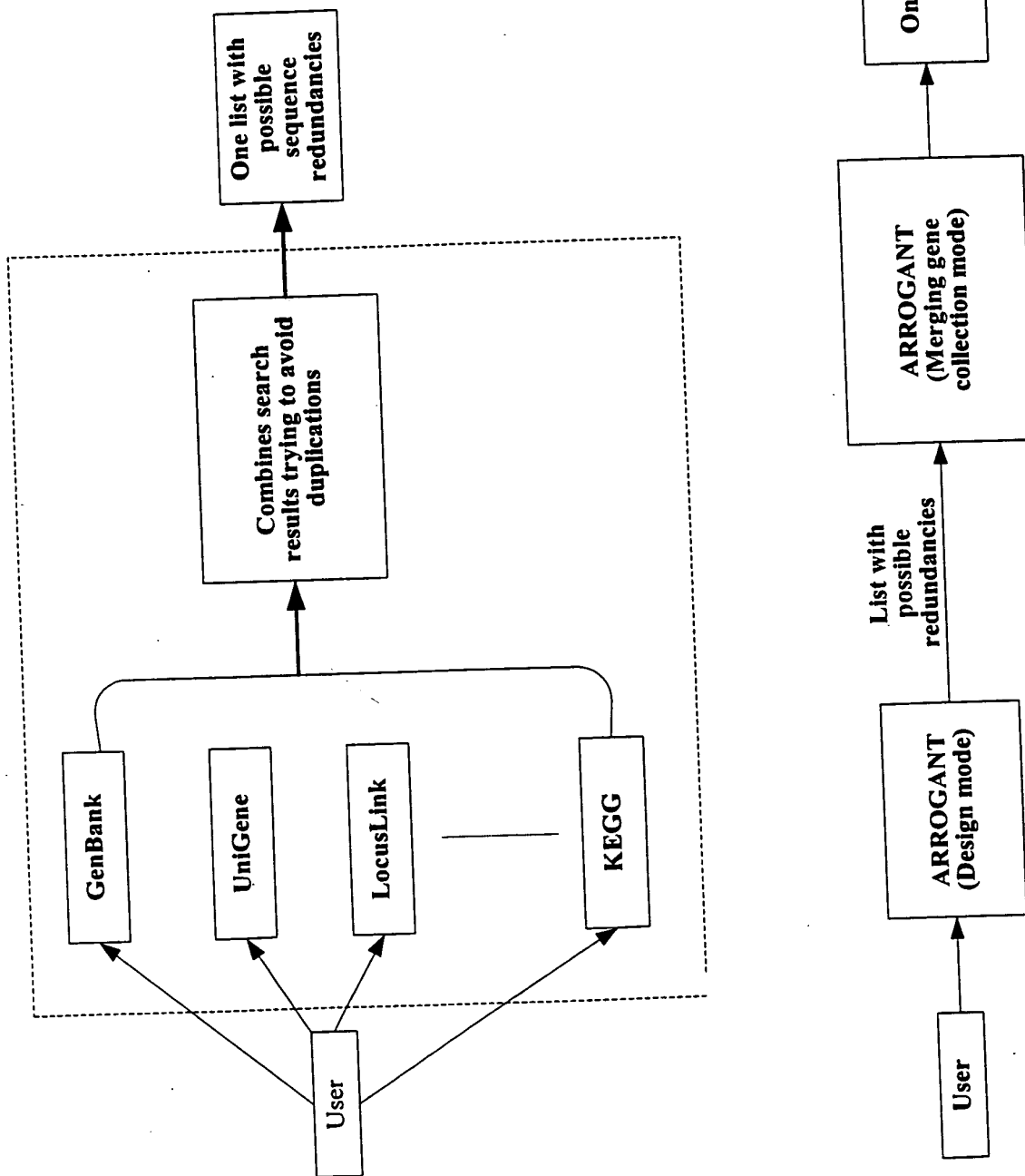


Fig 27

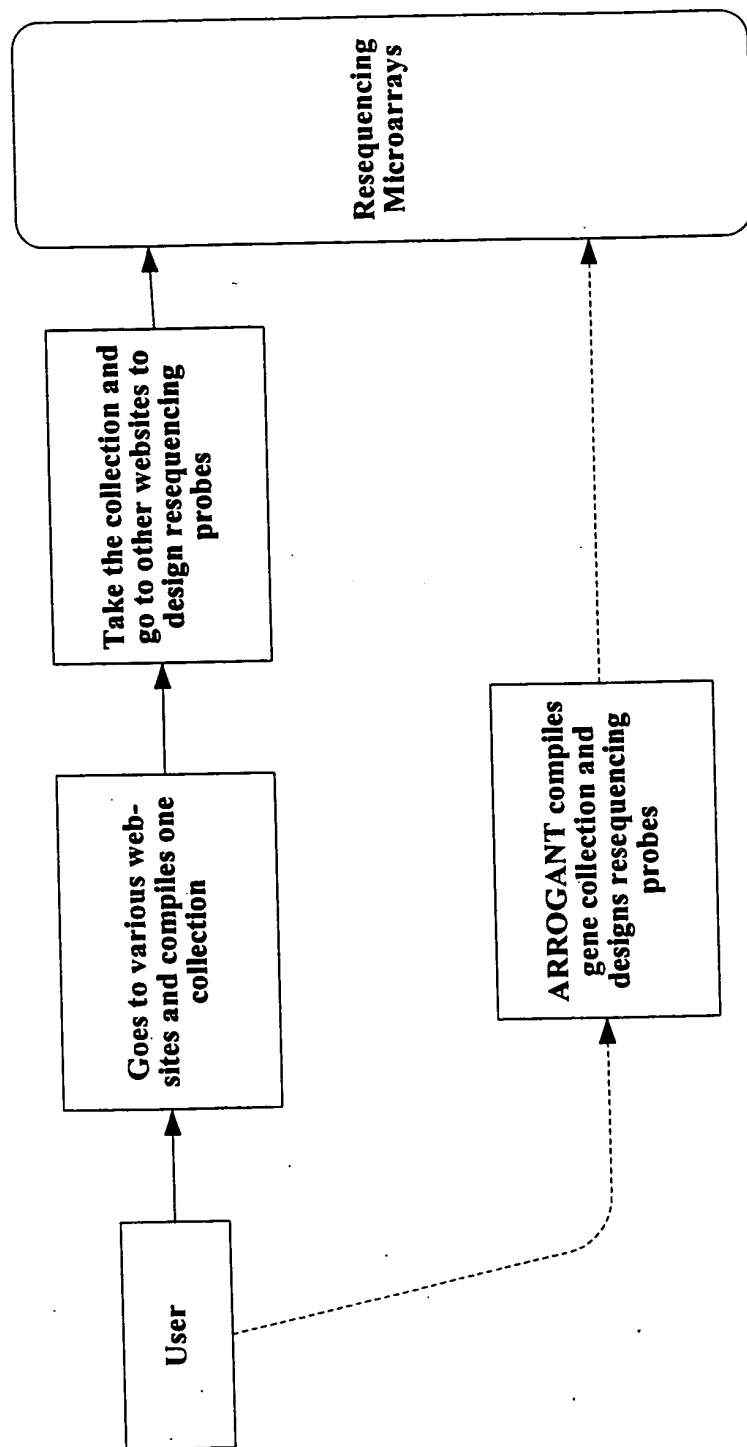


Fig 28

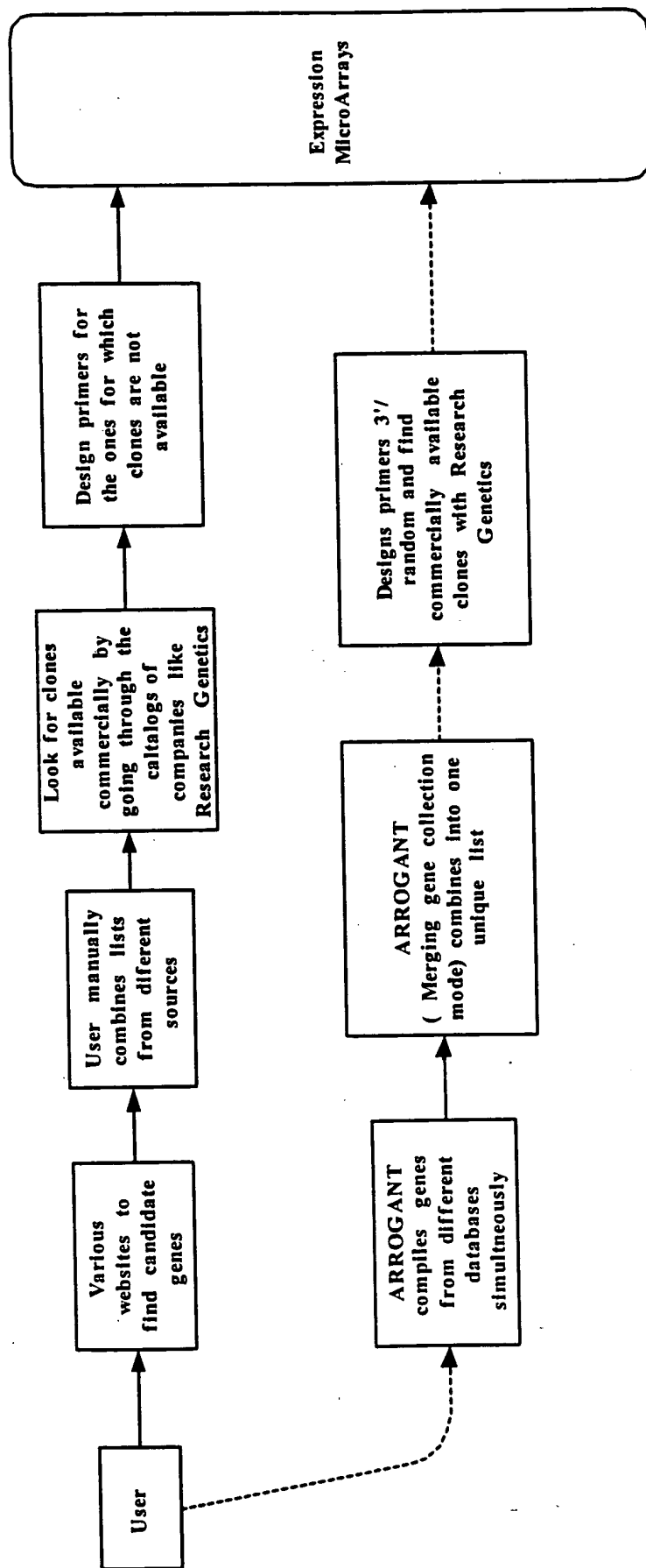


Fig 29

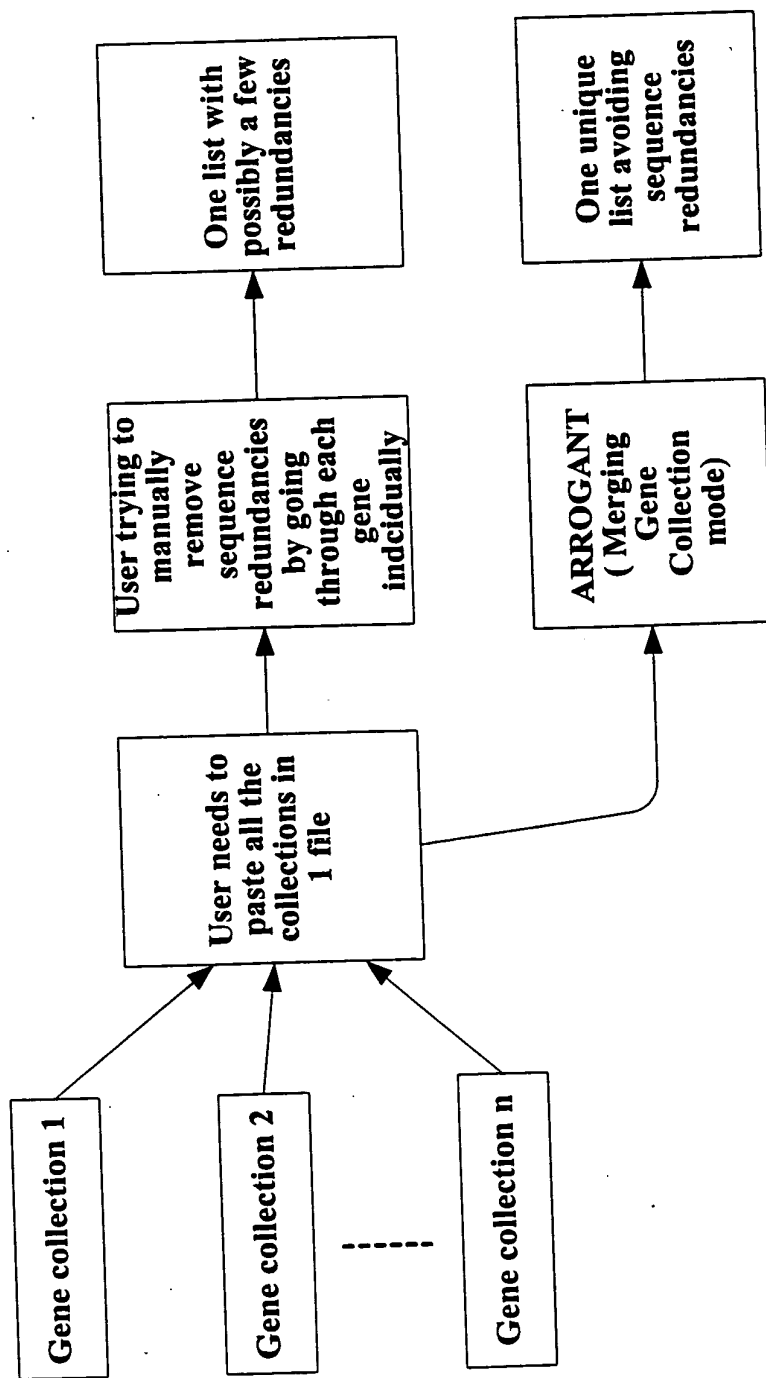


Fig 30

```
graph LR; A[Microarray results] --> B[Researcher interprets the results]; A -.-> C["ARROGANT (analysis mode) tags the potential false positives caused due to cross-hybridization"]; C -.-> B
```

```
graph LR; A[Members to be included on the expression micro-array] --> B[ARROGANT tags the regions causing potential cross-hybridization]; B --> C[Design primers to amplify sequences to be spotted on the microarray];
```

Members to be included on the expression micro-array

ARROGANT tags the regions causing potential cross-hybridization

Design primers to amplify sequences to be spotted on the microarray

Fig 31b